

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: MOSSAKOWSKA, Danuta Ewa Irena
COX, Vivienne Frances
SMITH, Richard Anthony Godwin
- (ii) TITLE OF INVENTION: COMPLEMENT RECEPTOR TYPE 1 (CR1)-LIKE
SEQUENCES
- (iii) NUMBER OF SEQUENCES: 64
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FOLEY & LARDNER
 - (B) STREET: 3000 K Street, N.W.
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/380,682
 - (B) FILING DATE: 19-OCT-1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: WO PCT/GB98/00727
 - (B) FILING DATE: 05-MAR-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9704519.9
 - (B) FILING DATE: 05-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: ISACSON, John P.
 - (B) REGISTRATION NUMBER: 33,715
 - (C) REFERENCE/DOCKET NUMBER: 88362/107
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	
1				5					10					15		
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	
			20					25					30			
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	
		35					40					45				
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	
	50					55					60					
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	
65					70				75						80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	
				85				90						95		
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
			100					105					110			
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	
		115					120					125				
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	
		130				135						140				
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	His	Cys	Asn	Leu	Gly	Ser	Arg	
145					150					155					160	
Gly	Lys	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	
				165				170						175		
Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	
			180					185					190			
Ile	Ile	Pro	Asn	Lys												
			195													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCAGTGCA	ACGCTCCGGA	ATGGCTGCCG	TTCGCGCGCC	CGACCAACCT	GA CTGATGAA	60
TTTGAGTTCC	CGATCGGTAC	CTACCTGAAC	TACGAATGCC	GCCCCGGGTTA	TAGCGGCCGC	120
CCGTTTTCTA	TCATCTGCCT	GAAAACTCT	GTCTGGACTG	GTGCTAAGGA	CCGTTGCCGA	180
CGTAAATCTT	GTCGTAATCC	GCCAGATCCG	GTTAACGGCA	TGGTGCATGT	GATCAAAGGC	240

ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC 300
TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT 360
TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCGCCA ACGGTGATTT CACCTCTATC 420
AGTCGCGAGT ATTTTCACTA TGGTTCTGTG GTGACCTACC ACTGCAATCT GGGTAGCCGT 480
GGTAAAAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG CAAAGACGAT 540
CAAGTGGGCA TCTGGAGCGG CCCGGCACC GAGTGCATCA TCCCGAACAA A 591

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CGACCATCGC CAACGGTGAT TTCACCTCTA TCAGTCGCGA GTATTTTCAC 50

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGAAAATAC TCGCGACTGA TAGAGGTGAA ATCACCGTTG GCGATGGTCG 50

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACCTACCAC TGCAATCTGG GTAGCCGTGG TAAAAAGGTG TTTGAGC 47

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCTCAAACAC CTTTTTACCA CGGCTACCCA GATTGCAGTG GTAGGTC

47

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCACTAGCAA AGACGATCAA GTGGG

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCCCTTGAT CGTCTTTGCT AGTGC

25

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	
1				5					10					15		
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	
			20					25					30			
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	
		35					40					45				
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	
		50				55					60					
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	
		65			70					75					80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	
				85				90						95		
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
			100					105					110			
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	
		115					120					125				
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	
		130				135						140				
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	
		145			150					155					160	
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	
			165						170					175		
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	
			180					185					190			
Ile	Ile	Pro	Asn	Lys												
			195													

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA	60
TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC	120
CCGTTTTCTA TCATCTGCCT GAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA	180
CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGATGT GATCAAAGGC	240

(2) INFORMATION FOR SEQ ID NO:11:

(A) LENGTH: 197 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

[illegible]

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

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ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA      60
TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC      120
CCGTTTTCTA TCATCTGCCT GAAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA      180
CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGATGT GATCAAAGGC      240
ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC      300
TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT      360
TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCACCA ACGGTGATTT CATCTCTACC      420
AATCGCGAGA ATTTTCACTA TGGTTCTGTG GTGACCTACC ACTGCAATCT GGGTAGCCGT      480
GGTAAAAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG TAATGACGAT      540
CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCCGAACAA A              591

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1          5          10          15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20          25          30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35          40          45
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50          55          60

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Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	65	70	75	80
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	85	90	95	
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	100	105	110	
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	115	120	125	
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	130	135	140	
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	145	150	155	160
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	165	170	175	
Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	180	185	190	
Ile	Ile	Pro	Asn	Lys												195			

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA	60
TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC	120
CCGTTTTCTA TCATCTGCCT GAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA	180
CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGCATGT GATCAAAGGC	240
ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC	300
TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT	360
TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCACCA ACGGTGATTT CATCTCTACC	420
AATCGCGAGA ATTTTCACTA TGGTTCTGTG GTGACCTACC GCTGCAATCC GGGTAGCGGT	480
GGTCGTAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG CAAAGACGAT	540
CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCCGAACAA A	591

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	1	5	10	15
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	20	25	30	
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	35	40	45	
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	50	55	60	
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	65	70	75	80
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	85	90	95	
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	100	105	110	
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	115	120	125	
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	130	135	140	
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	145	150	155	160
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	165	170	175	
Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	180	185	190	
Ile	Ile	Pro	Asn	Lys	195														

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA      60
TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC      120
CCGTTTTTCTA TCATCTGCCT GAAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA      180
CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGATGT GATCAAAGGC      240
ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC      300
TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT      360
TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCGCCA ACGGTGATTT CACCTCTATC      420
AGTCGCGAGT ATTTTCACTA TGGTTCTGTG GTGACCTACC GCTGCAATCC GGGTAGCGGT      480
GGTCGTAAGG TGTTTGAGCT CGTGGGTGAG GCGTCCATCT ACTGCACTAG CAAAGACGAT      540
CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCCGAACAA A              591

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1          5          10
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20        25        30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35        40        45
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50        55        60
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65        70        75
Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85        90        95
Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100       105       110
Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115       120       125

```

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
 145 150 155 160
 Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys
 195

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 591 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATGCAGTGCA ACGCTCCGGA ATGGCTGCCG TTCGCGCGCC CGACCAACCT GACTGATGAA 60
 TTTGAGTTCC CGATCGGTAC CTACCTGAAC TACGAATGCC GCCCGGGTTA TAGCGGCCGC 120
 CCGTTTTCTA TCATCTGCCT GAAAACTCT GTCTGGACTG GTGCTAAGGA CCGTTGCCGA 180
 CGTAAATCTT GTCGTAATCC GCCAGATCCG GTTAACGGCA TGGTGATGT GATCAAAGGC 240
 ATCCAGTTCG GTTCCCAAAT TAAATATTCT TGTACTAAAG GTTACCGTCT GATTGGTTCC 300
 TCCAGCGCTA CATGCATCAT CTCTGGTGAT ACTGTCATTT GGGATAATGA AACACCGATT 360
 TGTGACCGAA TTCCGTGTGG TCTGCCGCCG ACCATCACCA ACGGTGATTT CATCTCTACC 420
 AATCGCGAGA ATTTTCACTA TGGTTCTGTG GTGACCTACC ACTGCAATCT GGGTAGCCGT 480
 GGTAAAAGG TGTTTGAGCT CGTGGGTGAG CCGTCCATCT ACTGCACTAG CAAAGACGAT 540
 CAAGTGGGCA TCTGGAGCGG CCCGGCACCG CAGTGCATCA TCCCGAACAA A 591

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

Met Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
 1             5             10             15
Thr Ser Ile Ser Arg Glu Tyr Phe His Tyr Gly Ser Val Val Thr Tyr
          20             25             30
Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
          35             40             45
Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
 50             55             60
Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
65             70             75

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCGCCAACG GTGATTTTAC CTCTATCAGT      60
CGCGAGTATT TTTACTATGG TTCTGTGGTG ACCTACCGCT GCAATCCGGG TAGCGGTGGT      120
CGTAAGGTGT TTAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGTAA TGACGATCAA      180
GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA      228

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Thr Asn Gly Asp Phe
 1             5             10             15
Ile Ser Thr Asn Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr
          20             25             30
His Cys Asn Leu Gly Ser Arg Gly Lys Lys Val Phe Glu Leu Val Gly
          35             40             45

```

Glu Pro Ser Ile Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp
 50 55 60
 Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCACCAACG GTGATTTCAT CTCTACCAAT 60
 CGCGAGAATT TTCACTATGG TTCTGTGGTG ACCTACCACT GCAATCTGGG TAGCCGTGGT 120
 AAAAAGGTGT TTGAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGTAA TGACGATCAA 180
 GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA 228

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
 1 5 10 15
 Thr Ser Ile Ser Arg Glu Tyr Phe His Tyr Gly Ser Val Val Thr Tyr
 20 25 30
 Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
 35 40 45
 Glu Pro Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Ile Trp
 50 55 60
 Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCACCAACG GTGATTTTCAT CTCTACCAAT      60
CGCGAGAATT TTCACTATGG TTCTGTGGTG ACCTACCGCT GCAATCCGGG TAGCGGTGGT      120
CGTAAGGTGT TTGAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGCAA AGACGATCAA      180
GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA      228

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Met Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
 1              5              10              15
Thr Ser Ile Ser Arg Glu Tyr Phe His Tyr Gly Ser Val Val Thr Tyr
          20              25              30
Arg Cys Asn Pro Gly Ser Gly Gly Arg Lys Val Phe Glu Leu Val Gly
          35              40              45
Glu Pro Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Ile Trp
          50              55              60
Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
          65              70              75

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCGCCAACG GTGATTTTCAC CTCTATCAGT      60

```

CGCGAGTATT TTCACTATGG TTCTGTGGTG ACCTACCGCT GCAATCCGGG TAGCGGTGGT 120
 CGTAAGGTGT TTGAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGCAA AGACGATCAA 180
 GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA 228

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe
1				5					10					15	
Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr
			20					25					30		
His	Cys	Asn	Leu	Gly	Ser	Arg	Gly	Lys	Lys	Val	Phe	Glu	Leu	Val	Gly
		35					40					45			
Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp
	50					55					60				
Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro	Asn	Lys				
65					70					75					

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCACCAACG GTGATTTTCAT CTCTACCAAT 60
 CGCGAGAATT TTCACTATGG TTCTGTGGTG ACCTACCACT GCAATCTGGG TAGCCGTGGT 120
 AAAAAGGTGT TTGAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGCAA AGACGATCAA 180
 GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA 228

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Met Arg Ile Pro Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe
1           5           10           15
Thr Ser Ile Ser Arg Glu Tyr Phe His Tyr Gly Ser Val Val Thr Tyr
          20           25           30
His Cys Asn Leu Gly Ser Arg Gly Lys Lys Val Phe Glu Leu Val Gly
          35           40           45
Glu Pro Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Ile Trp
          50           55           60
Ser Gly Pro Ala Pro Gln Cys Ile Ile Pro Asn Lys
          65           70           75

```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

ATGCGAATTC CGTGTGGTCT GCCGCCGACC ATCGCCAACG GTGATTTTAC CTCTATCAGT      60
CGCGAGTATT TTCACTATGG TTCTGTGGTG ACCTACCACT GCAATCTGGG TAGCCGTGGT      120
AAAAAGGTGT TTGAGCTCGT GGGTGAGCCG TCCATCTACT GCACTAGCAA AGACGATCAA      180
GTGGGCATCT GGAGCGGCCC GGCACCGCAG TGCATCATCC CGAACAAA      228

```

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15
 Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30
 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45
 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60
 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
 145 150 155 160
 Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Cys
 195

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTGGAGCGGG CCCGCACCGC AGTGCATCAT CCCGAACAAA TGCTAATAAA AGC

53

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCTTTTATTA GCATTTGTTC GGGATGATGC ACTGCGGTGC GGGCCCGCTC CAG

53

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	1	5	10	15
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	20	25	30	
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	35	40	45	
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	50	55	60	
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	65	70	75	80
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	85	90	95	
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	100	105	110	
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	115	120	125	
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	130	135	140	
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	His	Cys	Asn	Leu	Gly	Ser	Arg	145	150	155	160
Gly	Lys	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	165	170	175	
Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	180	185	190	
Ile	Ile	Pro	Asn	Lys	Cys	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Lys	195	200	205	

Ser Pro Ser Lys Ser Ser Gly
210 215

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15
Cys

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gln Cys Asn Val Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15
Leu Thr Asp Asp Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45
Asn Ser Val Trp Thr Ser Ala Lys Asp Lys Cys Lys Arg Lys Ser Cys
50 55 60
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Ala His Val Ile Lys Asp
65 70 75 80
Ile Gln Phe Arg Ser Gln Ile Lys Tyr Ser Cys Pro Lys Gly Tyr Arg
85 90 95
Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asn Thr Val
100 105 110
Ile Trp Asp Asn Lys Thr Pro Val Cys Asp Arg Ile Ile Cys Gly Leu
115 120 125

Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
 145 150 155 160

Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Cys
 195

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAGTGCAACG TGCCGGAATG G

21

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CCATTCCGGA ACGTTGCACT G

21

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GACTGATGAT TTTGAGTTCC

20

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GGAACTCAAA ATCATCAGTC

20

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GTCTGGACTA GTGCTAAGGA CAAGTGCAAA CGTAAATCTT GTCG

44

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

CGACAAGATT TACGTTTGCA CTTGTCCTTA GCACTAGTCC AGAC

44

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCATGGCG CATGTGATCA AAGATATCCA GTTCCGATCG CAAATTAAAT ATTCTTGTCC 60
 TAAGGGTTAC CGTC 74

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GACGGTAACC CTTAGGACAA GAATATTTAA TTTGCGATCG GAACTGGATA TCTTTGATCA 60
 CATGCGCCAT GCCG 74

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CATCTCTGGT AATACTGTCA TTTGGGATAA TAAACACCG GTTTGTGACC 50

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGTCACAAAC CGGTGTTTTA TTATCCCAA TGACAGTATT ACCAGAGATG 50

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

21

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met 1	Gln	Cys	Asn	Val 5	Pro	Glu	Trp	Leu	Pro 10	Phe	Ala	Arg	Pro	Thr 15	Asn
Leu	Thr	Asp	Asp 20	Phe	Glu	Phe	Pro	Ile 25	Gly	Thr	Tyr	Leu	Asn 30	Tyr	Glu
Cys	Arg	Pro 35	Gly	Tyr	Ser	Gly	Arg 40	Pro	Phe	Ser	Ile	Ile 45	Cys	Leu	Lys
Asn	Ser 50	Val	Trp	Thr	Ser	Ala 55	Lys	Asp	Lys	Cys	Lys 60	Arg	Lys	Ser	Cys
Arg 65	Asn	Pro	Pro	Asp 70	Pro	Val	Asn	Gly	Met 75	Ala	His	Val	Ile	Lys	Asp 80
Ile	Gln	Phe	Arg	Ser 85	Gln	Ile	Lys	Tyr	Ser 90	Cys	Pro	Lys	Gly	Tyr 95	Arg

```

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asn Thr Val
      100      105      110

Ile Trp Asp Asn Lys Thr Pro Val Cys Asp Arg Ile Ile Cys Gly Leu
      115      120      125

Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
      130      135      140

Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
      145      150      155      160

Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
      165      170      175

Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
      180      185      190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
      195      200      205

Ser Pro Ser Lys Ser Ser Gly
      210      215

```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Gln Cys Asn Val Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1          5          10          15

Leu Thr Asp Asp Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
      20          25          30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
      35          40          45

Asn Ser Val Trp Thr Ser Ala Lys Asp Lys Cys Lys Arg Lys Ser Cys
      50          55          60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Ala His Val Ile Lys Asp
      65          70          75          80

Ile Gln Phe Arg Ser Gln Ile Lys Tyr Ser Cys Pro Lys Gly Tyr Arg
      85          90          95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asn Thr Val
      100      105      110

Ile Trp Asp Asn Lys Thr Pro Val Cys Asp Arg Ile Pro Cys Gly Leu
      115      120      125

```



```

Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
130          135          140

Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
145          150          155          160

Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
          165          170          175

Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
          180          185          190

Ile Ile Pro Asn Lys Cys
          195

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Met Gln Cys Asn Val Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1          5          10          15

Leu Thr Asp Asp Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
          20          25          30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
          35          40          45

Asn Ser Val Trp Thr Ser Ala Lys Asp Lys Cys Lys Arg Lys Ser Cys
          50          55          60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Ala His Val Ile Lys Asp
          65          70          75          80

Ile Gln Phe Arg Ser Gln Ile Lys Tyr Ser Cys Pro Lys Gly Tyr Arg
          85          90          95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asn Thr Val
          100          105          110

Ile Trp Asp Asn Lys Thr Pro Val Cys Asp Arg Ile Pro Cys Gly Leu
          115          120          125

Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
          130          135          140

Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
          145          150          155          160

Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
          165          170          175

```

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

CGCACC GCAG TGCATCATCC CGAACAAAGA TGGCCCGAGC GAAATTCTGC GTGGCGATTT 60
TAGCAGCTGC TA 72

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGCTTAGCAG CTGCTAAAT CGCCACGCAG AATTCGCTC GGGCCATCTT TGTTCGGGAT 60
GATGCACTGC GGTGCGGGCC 80

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	
			20					25					30			
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	
		35					40					45				
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	
	50					55					60					
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	
65					70				75						80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	
			85					90						95		
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
			100					105					110			
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	
		115					120					125				
Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	
		130				135					140					
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	His	Cys	Asn	Leu	Gly	Ser	Arg	
145					150					155					160	
Gly	Lys	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	
				165					170					175		
Ser	Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	
			180					185					190			
Ile	Ile	Pro	Asn	Lys	Asp	Gly	Pro	Ser	Glu	Ile	Leu	Arg	Gly	Asp	Phe	
		195				200						205				
Ser	Ser	Cys														
		210														

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 84 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGCACCGCAG TGCATCATCC CGAACAAAGC GGCGCCCAGC GTGATTGGCT TCCGTATTCT	60
GCTGCTGAAA GTGGCGGGCT GATA	84

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AGCTTATCAG CCCGCCACTT TCAGCAGCAG AATACGGAAG CCAATCACGC TGGGCGCCGC 60

TTTGTTCGGG ATGATGCACT GCGGTGCGGG CC 92

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 214 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Ala Asn Gly Asp Phe Thr Ser Ile Ser Arg Glu Tyr
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr His Cys Asn Leu Gly Ser Arg
145 150 155 160

Gly Lys Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Lys Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu
 195 200 205

Leu Leu Lys Val Ala Gly
 210

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 438 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gln	Cys	Asn	Val	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	1	5	10	15
Thr	Asp	Asp	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	20	25	30	
Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn	35	40	45	
Ser	Val	Trp	Thr	Ser	Ala	Lys	Asp	Lys	Cys	Lys	Arg	Lys	Ser	Cys	Arg	50	55	60	
Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Ala	His	Val	Ile	Lys	Asp	Ile	65	70	75	80
Gln	Phe	Arg	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Pro	Lys	Gly	Tyr	Arg	Leu	85	90	95	
Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asn	Thr	Val	Ile	100	105	110	
Trp	Asp	Asn	Lys	Thr	Pro	Val	Cys	Asp	Arg	Ile	Ile	Cys	Gly	Leu	Pro	115	120	125	
Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Thr	Ser	Ile	Ser	Arg	Glu	Tyr	Phe	130	135	140	
His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	His	Cys	Asn	Leu	Gly	Ser	Arg	Gly	145	150	155	160
Lys	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	165	170	175	
Lys	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	180	185	190	
Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val	195	200	205	
Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	Phe	Arg	210	215	220	

Cys 225	Gln	Pro	Gly	Phe	Gly 230	Met	Lys	Gly	Pro	Ser 235	His	Val	Lys	Cys	Gln 240
Ala	Leu	Asn	Lys	Trp 245	Glu	Pro	Glu	Leu	Pro 250	Ser	Cys	Ser	Arg	Val 255	Cys
Gln	Pro	Pro	Pro	Asp 260	Val	Leu	His	Ala 265	Glu	Arg	Thr	Gln	Arg 270	Asp	Lys
Asp	Asn	Phe 275	Ser	Pro	Gly	Gln	Glu 280	Val	Phe	Tyr	Ser	Cys 285	Glu	Pro	Gly
Tyr 290	Asp	Leu	Arg	Gly	Ser	Thr 295	Tyr	Leu	His	Cys	Thr 300	Pro	Gln	Gly	Asp
Trp 305	Ser	Pro	Ala	Ala	Pro 310	Arg	Cys	Glu	Val	Lys 315	Ser	Cys	Asp	Asp	Phe 320
Leu	Gly	Gln	Leu	Pro 325	Asn	Gly	His	Val	Leu 330	Phe	Pro	Leu	Asn	Leu 335	Gln
Leu	Gly	Ala	Lys 340	Val	Asp	Phe	Val	Cys 345	Asp	Glu	Gly	Phe	Gln 350	Leu	Lys
Gly	Ser	Ser 355	Ala	Ser	Tyr	Cys	Val 360	Leu	Ala	Gly	Met	Glu 365	Ser	Leu	Trp
Asn 370	Ser	Ser	Val	Pro	Val	Cys 375	Glu	Arg	Glu	Ser	Cys 380	Lys	Thr	Pro	Pro
Val 385	Pro	Val	Asn	Gly	Met 390	Val	His	Val	Ile	Thr 395	Asp	Ile	His	Val	Gly 400
Ser	Arg	Ile	Asn 405	Tyr	Ser	Cys	Thr	Thr	Gly 410	His	Arg	Leu	Ile	Gly 415	His
Ser	Ser	Ala	Glu 420	Cys	Ile	Leu	Ser	Gly 425	Asn	Thr	Ala	His	Trp 430	Ser	Met
Lys	Pro	Pro	Ile	Cys	Gln										
					435										

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Val 1	Gly	Pro	Pro	Ala	Pro	Gly	Leu	Pro	Phe 10	Cys	Cys	Gly	Gly	Ser 15	Leu
Leu	Ala	Val	Val	Val	Leu	Leu	Ala	Leu	Pro	Val	Ala	Trp	Gly 30	Gln	Cys
			20					25							

Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	Leu	Thr	Asp	35	40	45
Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	Cys	Arg	Pro	50	55	60
Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	Asn	Ser	Val	65	70	75
Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	Arg	Asn	Pro	85	90	95
Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	Ile	Gln	Phe	100	105	110
Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	Leu	Ile	Gly	115	120	125
Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	Ile	Trp	Asp	130	135	140
Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	Pro	Pro	Thr	145	150	155
Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	Phe	His	Tyr	165	170	175
Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	Gly	Arg	Lys	180	185	190
Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	Ser	Asn	Asp	195	200	205
Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	Ile	Ile	Pro	210	215	220
Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	Leu	Val	Ser	Asp	225	230	235
Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	Phe	Arg	Cys	Gln	245	250	255
Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	Cys	Gln	Ala	Leu	260	265	270
Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	Val	Cys	Gln	Pro	275	280	285
Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	Asp	Lys	Asp	Asn	290	295	300
Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	Pro	Gly	Tyr	Asp	305	310	315
Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	Gly	Asp	Trp	Ser	325	330	335
Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	Asp	Phe	Met	Gly	340	345	350
Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	Leu	Gln	Leu	Gly	355	360	365

Ala	Lys	Val	Asp	Phe	Val	Cys	Asp	Glu	Gly	Phe	Gln	Leu	Lys	Gly	Ser
370						375					380				
Ser	Ala	Ser	Tyr	Cys	Val	Leu	Ala	Gly	Met	Glu	Ser	Leu	Trp	Asn	Ser
385					390					395					400
Ser	Val	Pro	Val	Cys	Glu	Gln	Ile	Phe	Cys	Pro	Ser	Pro	Pro	Val	Ile
				405					410					415	
Pro	Asn	Gly	Arg	His	Thr	Gly	Lys	Pro	Leu	Glu	Val	Phe	Pro	Phe	Gly
			420					425					430		
Lys	Ala	Val	Asn	Tyr	Thr	Cys	Asp	Pro	His	Pro	Asp	Arg	Gly	Thr	Ser
	435						440					445			
Phe	Asp	Leu	Ile	Gly	Glu	Ser	Thr	Ile	Arg	Cys	Thr	Ser	Asp	Pro	Gln
450						455					460				
Gly	Asn	Gly	Val	Trp	Ser	Ser	Pro	Ala	Pro	Arg	Cys	Gly			
465					470					475					

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Lys	Ser	Pro	Ser	Lys	Ser	Ser	Gly
1			5						10					15	

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gly	Ser	Ser	Lys	Ser	Pro	Ser	Lys	Lys	Lys	Lys	Lys	Lys	Pro	Gly	Asp
1			5						10					15	

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Asn Ser Asn Glu Thr Pro Lys Lys Lys Lys Lys Arg Phe Ser Phe
 1 5 10 15

Lys Lys Ser Gly
 20

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Gly Arg Gly Asp Ser Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr
 1 5 10 15

Ala